SEQUENCE LISTING

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<120> POLYNUCLEOTIDE ENCODING AN ACTIVATED HUMAN T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN CONJUGATING ENZYME

<130> D0034np

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<150> 60/308,706
<151> 2001-07-30

<150> 60/244,688
<151> 2000-10-30

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gggccgatcg cacgcccccc gtggcggcga cgacccattc gaacgtctgc cctatcaact 240

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Gln Gly Gln Gln Gln Pro Gly Pro Gly Gln Gln Leu Gly Gly Gln Gly
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Ala Ala Pro Gly Ala Gly Gly Gly Pro Gly Gly Gly Pro Gly Pro Gly
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ccc tgc ctg agg cga gag ctg aag ctg ctc gag tcc atc ttc cac cgc 678
Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu Glu Ser Ile Phe His Arg
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ggc cac gag cgc ttc cgc att gcc agc gcc tgc ctg gac gag ctg agc 726
Gly His Glu Arg Phe Arg Ile Ala Ser Ala Cys Leu Asp Glu Leu Ser
55 60 65 70

tgc gag ttc ctg ctg gct ggg gcc gga ggg gcc ggg gcg ggg gcc gcg 774
Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly Ala Gly Ala Gly Ala Ala
75 80 85

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Pro Gly Pro His Leu Pro Pro Arg Gly Ser Val Pro Gly Asp Pro Val
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cgc atc cac tgc aac atc acg gag tca tac cct gct gtg ccc ccc atc 870
Arg Ile His Cys Asn Ile Thr Glu Ser Tyr Pro Ala Val Pro Pro Ile
105 110 115

tgg tcg gtg gag tct gat gac cct aac ttg gct gct gtc ttg gag agg 918
Trp Ser Val Glu Ser Asp Asp Pro Asn Leu Ala Ala Val Leu Glu Arg
120 125 130

ctg gtg gac ata aag aaa ggg aat act ctg cta ttg cag cat ctg aag 966
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135 140 145 150

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Arg Ile Ile Ser Asp Léu Cys Lys Leu Tyr Asn Leu Pro Gln His Pro
155 160 165

gat gtg gag atg ctg gat caa ccc ttg cca gca gag cag tgc aca cag 1062
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170 175 180

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Glu Asp Val Ser Ser Glu Asp Glu Asp Glu Glu Met Pro Glu Asp Thr
185 190 195

gaa gac tta gat cac tat gaa atg aaa gag gaa gag cca gct gag ggc 1158
Glu Asp Leu Asp His Tyr Glu Met Lys Glu Glu Glu Pro Ala Glu Gly
200 205 210

aag aaa tct gaa gat gat ggc att gga aaa gaa aac ttg gcc atc cta 1206
Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys Glu Asn Leu Ala Ile Leu
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gag aaa att aaa aag aac cag agg caa gat tac tta aat ggt gca gtg   1254
Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp Tyr Leu Asn Gly Ala Val
                235                 240                 245

tct ggc tcg gtg cag gcc act gac cgg ctg atg aag gag ctc agg gat   1302
Ser Gly Ser Val Gln Ala Thr Asp Arg Leu Met Lys Glu Leu Arg Asp
            250                 255                 260

ata tac cga tca cag agt ttc aaa ggc gga aac tat gca gtc gaa ctc   1350
Ile Tyr Arg Ser Gln Ser Phe Lys Gly Gly Asn Tyr Ala Val Glu Leu
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gtg aat gac agt ctg tat gat tgg aat gtc aaa ctc ctc aaa gtt gac   1398
Val Asn Asp Ser Leu Tyr Asp Trp Asn Val Lys Leu Leu Lys Val Asp
    280                 285                 290

cag gac agc gct ttg cac aac gat ctc cag atc ctc aaa gag aaa gaa   1446
Gln Asp Ser Ala Leu His Asn Asp Leu Gln Ile Leu Lys Glu Lys Glu
295                 300                 305                 310

gga gcc gac ttc att cta ctt aac ttt tcc ttt aaa gat aac ttt ccc   1494
Gly Ala Asp Phe Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro
                315                 320                 325

ttt gac cca cca ttt gtc agg gtt gtg tct cca gtc ctc tct gga ggg   1542
Phe Asp Pro Pro Phe Val Arg Val Val Ser Pro Val Leu Ser Gly Gly
            330                 335                 340

tat gtt ctg ggc gga ggg gcc atc tgc atg gaa ctt ctc acc aaa cag   1590
Tyr Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr Lys Gln
        345                 350                 355

ggc tgg agc agt gcc tac tcc ata gag tca gtg atc atg cag atc agt   1638
Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser Val Ile Met Gln Ile Ser
    360                 365                 370

gcc aca ctg gtg aag ggg aaa gca cga gtg cag ttt gga gcc aac aaa   1686
Ala Thr Leu Val Lys Gly Lys Ala Arg Val Gln Phe Gly Ala Asn Lys
375                 380                 385                 390

tct caa tac agt ctg aca aga gca cag cag tcc tac aag tcc ttg gtg   1734
Ser Gln Tyr Ser Leu Thr Arg Ala Gln Gln Ser Tyr Lys Ser Leu Val
                395                 400                 405

cag atc cac gaa aaa aac ggc tgg tac aca ccc cca aaa gaa gac ggc   1782
Gln Ile His Glu Lys Asn Gly Trp Tyr Thr Pro Pro Lys Glu Asp Gly
            410                 415                 420

taaccctgga gtatcaccct tcctccctcc ccaggcacca ctggaccaat tacctttgaa 1842

tgctgtattt ggatctcacg ctgcctctgt ggttccctcc ctcatttttc ctggacgtga 1902

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acagaactgt ttcaagtact caagactgac ttacagacca accaaccacc ttgctggaac 2022

ccttgctagc aggcattctt ataaaagaaa ctttcgagcc tccttatatt gctggaaact 2082
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<213> Homo sapiens

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             20                  25                  30

Gly Gly Pro Gly Pro Gly Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu
         35                  40                  45

Glu Ser Ile Phe His Arg Gly His Glu Arg Phe Arg Ile Ala Ser Ala
     50                  55                  60

Cys Leu Asp Glu Leu Ser Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly
 65                  70                  75                  80

Ala Gly Ala Gly Ala Ala Pro Gly Pro His Leu Pro Pro Arg Gly Ser
                 85                  90                  95

Val Pro Gly Asp Pro Val Arg Ile His Cys Asn Ile Thr Glu Ser Tyr
            100                 105                 110

Pro Ala Val Pro Pro Ile Trp Ser Val Glu Ser Asp Asp Pro Asn Leu
        115                 120                 125

Ala Ala Val Leu Glu Arg Leu Val Asp Ile Lys Lys Gly Asn Thr Leu
    130                 135                 140

Leu Leu Gln His Leu Lys Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr
145                 150                 155                 160

Asn Leu Pro Gln His Pro Asp Val Glu Met Leu Asp Gln Pro Leu Pro
                165                 170                 175

Ala Glu Gln Cys Thr Gln Glu Asp Val Ser Ser Glu Asp Glu Asp Glu
            180                 185                 190

Glu Met Pro Glu Asp Thr Glu Asp Leu Asp His Tyr Glu Met Lys Glu
        195                 200                 205

Glu Glu Pro Ala Glu Gly Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys
    210                 215                 220

Glu Asn Leu Ala Ile Leu Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp
225                 230                 235                 240
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Tyr Leu Asn Gly Ala Val Ser Gly Ser Val Gln Ala Thr Asp Arg Leu
245 250 255

Met Lys Glu Leu Arg Asp Ile Tyr Arg Ser Gln Ser Phe Lys Gly Gly
260 265 270

Asn Tyr Ala Val Glu Leu Val Asn Asp Ser Leu Tyr Asp Trp Asn Val
275 280 285

Lys Leu Leu Lys Val Asp Gln Asp Ser Ala Leu His Asn Asp Leu Gln
290 295 300

Ile Leu Lys Glu Lys Glu Gly Ala Asp Phe Ile Leu Leu Asn Phe Ser
305 310 315 320

Phe Lys Asp Asn Phe Pro Phe Asp Pro Pro Phe Val Arg Val Val Ser
325 330 335

Pro Val Leu Ser Gly Gly Tyr Val Leu Gly Gly Gly Ala Ile Cys Met
340 345 350

Glu Leu Leu Thr Lys Gln Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser
355 360 365

Val Ile Met Gln Ile Ser Ala Thr Leu Val Lys Gly Lys Ala Arg Val
370 375 380

Gln Phe Gly Ala Asn Lys Ser Gln Tyr Ser Leu Thr Arg Ala Gln Gln
385 390 395 400

Ser Tyr Lys Ser Leu Val Gln Ile His Glu Lys Asn Gly Trp Tyr Thr
405 410 415

Pro Pro Lys Glu Asp Gly
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<213> Caenorhabditis elegans

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Asp Glu Leu Ser Met Lys Phe Ile Asn Ala Glu Asn Lys Gly Ile Ile
35 40 45

Val Thr Ala Asn Ile Gln Glu Asn Tyr Pro Arg Gln Pro Pro Ile Trp
50 55 60

Phe Ser Glu Ser Asp Asp Val Pro Val Ile Gly Met Ser Leu Gln Arg
65 70 75 80

Leu Thr Glu Thr Glu Glu Ser Thr Asn Ile Leu His Gln Val His Arg
85 90 95

Leu Val Ser Asp Leu Cys Ser Phe Tyr Asn Leu Gln Met Pro Cys Glu
100 105 110

Leu Pro Gln Ile Ala Pro Pro Val Arg Asp Asp Ile Asp Glu Gly Arg
115 120 125

Gly Ser Asp Ile Ser Asp Thr Thr Ser Glu Pro Ile Asp Asp Asp Met
130 135 140

Ala Gly Asp Gly Glu Val Asp Asp Asp Asp Glu Glu Glu Glu Asp Asp
145 150 155 160

Glu Asp Ala Asp Gly Asp Ile Glu Ile Val Glu Met Ala Glu Glu Asp
165 170 175

Pro Thr Ser Gln His Asp Val Gly Val Ser Lys Glu Gly Leu Asp Met
180 185 190

Leu Asp Lys Val Ser Lys Ile Asn Arg Gln Gln His Leu Asp Gly Lys
195 200 205

Val Gln Gly Ser Ile Thr Ala Thr Asp Arg Leu Met Lys Glu Ile Arg
210 215 220

Asp Ile His Arg Ser Glu His Phe Lys Asn Gly Ile Tyr Thr Phe Glu
225 230 235 240

Leu Glu Lys Glu Glu Asn Leu Tyr Gln Trp Trp Ile Lys Leu His Lys
245 250 255

Val Asp Glu Asp Ser Pro Leu Phe Glu Asp Met Lys Lys Leu Lys Lys
260 265 270

Asp His Asn Gln Asp His Leu Leu Phe Ser Phe Thr Phe Asn Glu Lys
275 280 285

Phe Pro Cys Asp Pro Pro Phe Val Arg Val Val Ala Pro His Ile Asn
290 295 300

Gln Gly Phe Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr
305 310 315 320

Lys Gln Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser Cys Ile Leu Gln
325 330 335

Ile Ala Ala Thr Leu Val Lys Gly Arg Ala Arg Ile Ser Phe Asp Ala
340 345 350

Lys His Thr Ser Thr Tyr Ser Met Ala Arg Ala Gln Gln Ser Phe Lys
355 360 365

Ser Leu Gln Gln Ile His Ala Lys Ser Gly Cys Thr Phe Leu Cys Ser
370 375 380

Thr Pro Ser Ser His Phe Phe Ala Leu His Leu Val Phe Phe Leu His
385 390 395 400

Ser Asp Asp Phe Phe Phe Asn Gly Phe Leu Lys Ser Glu Thr Phe Thr
405 410 415

Phe Phe Lys Leu Ser Phe Arg Gly Tyr Ile Ser Ser Leu Val Leu Tyr
420 425 430

Ser Phe Ser Arg His Leu His His Pro Phe Phe Thr Arg Phe Leu Ile
435 440 445

Pro Gln Leu Gln Pro Pro Pro Ile Pro Phe Gln Leu Ile Pro Pro Phe
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Leu Asn Arg Thr Lys His Val
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<213> Drosophila melanogaster

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Asp Glu Leu Leu Cys Arg Phe Ile Asp Lys Asn Gly Lys Arg Tyr Asp
35 40 45

Ile His Ala Asn Ile Thr Glu Thr Tyr Pro Ser Ser Pro Pro Val Trp
50 55 60

Phe Ala Glu Ser Glu Glu Thr Ser Val Thr Asn Ala Val Gln Ile Leu
65 70 75 80

Ser Asn Thr Asn Gly Arg Asp Asn His Val Ile Asn Gln Val Gly Ile
85 90 95

Leu Leu Arg Glu Leu Cys Arg Leu His Asn Val Pro Leu Pro Pro Asp
100 105 110

Ile Asp Asn Leu Ala Leu Pro Leu Gln Thr Pro Pro Pro Ser Ala Ser
115 120 125

Pro Leu Arg Cys Glu Gln Arg Pro Gly Gly Gly Gly Ala Gly Gly Gly
130 135 140

Gly Gly Pro His Gly Asn Glu Glu Thr Asp Ser Asp Gln Glu Glu Ile
145 150 155 160

Glu Asp Pro Ile Gly Glu Ser Glu Gln Glu Ser Glu Gly Asp Glu Asp
165 170 175

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Leu Pro Leu Glu Met Asp Asp Val Arg Ser Thr Ser Lys Lys Asp Asp
            180                 185                 190

Met Glu Val Glu His Leu Ala Thr Leu Glu Lys Leu Arg Gln Ser Gln
        195                 200                 205

Arg Gln Asp Tyr Leu Lys Gly Ser Val Ser Gly Ser Val Gln Ala Thr
    210                 215                 220

Asp Arg Leu Met Lys Glu Leu Arg Asp Ile Tyr Arg Ser Asp Ala Phe
225                 230                 235                 240

Lys Lys Asn Met Tyr Ser Ile Glu Leu Val Asn Glu Ser Ile Tyr Glu
                245                 250                 255

Trp Asn Ile Arg Leu Lys Ser Val Asp Pro Asp Ser Pro Leu His Ser
            260                 265                 270

Asp Leu Gln Met Leu Lys Glu Lys Glu Gly Lys Asp Ser Ile Leu Leu
        275                 280                 285

Asn Ile Leu Phe Lys Glu Thr Tyr Pro Phe Glu Pro Pro Phe Val Arg
    290                 295                 300

Val Val His Pro Ile Ile Ser Gly Gly Tyr Val Leu Ile Gly Gly Ala
305                 310                 315                 320

Ile Cys Met Glu Leu Leu Thr Lys Gln Gly Trp Ser Ser Ala Tyr Thr
                325                 330                 335

Val Glu Ala Val Ile Met Gln Ile Ala Ala Thr Leu Val Lys Gly Lys
            340                 345                 350

Ala Arg Ile Gln Phe Gly Ala Thr Lys Ala Leu Thr Gln Gly Gln Tyr
        355                 360                 365

Ser Leu Ala Arg Ala Gln Gln Ser Phe Lys Ser Leu Val Gln Ile His
    370                 375                 380

Glu Lys Asn Gly Trp Phe Thr Pro Pro Lys Glu Asp Gly
385                 390                 395


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<213> Mus musculus

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Glu Glu Gln Glu Glu Arg Lys Pro Ser Ala Thr Gln Gln Lys Lys Asn
         35                  40                  45
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Thr Lys Leu Ser Ser Lys Thr Thr Ala Lys Leu Ser Thr Ser Ala Lys
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Arg Ile Gln Lys Glu Leu Ala Glu Ile Thr Leu Asp Pro Pro Pro Asn
 65                  70                  75                  80

Cys Ser Ala Gly Pro Lys Gly Asp Asn Ile Tyr Glu Trp Arg Ser Thr
                 85                  90                  95

Ile Leu Gly Pro Pro Gly Ser Val Tyr Glu Gly Gly Val Phe Phe Leu
            100                 105                 110

Asp Ile Thr Phe Ser Ser Asp Tyr Pro Phe Lys Pro Pro Lys Val Thr
        115                 120                 125

Phe Arg Thr Arg Ile Tyr His Cys Asn Ile Asn Ser Gln Gly Val Ile
    130                 135                 140

Cys Leu Asp Ile Leu Lys Asp Asn Trp Ser Pro Ala Leu Thr Ile Ser
145                 150                 155                 160

Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Cys Asn Pro Ala
                165                 170                 175

Asp Pro Leu Val Gly Ser Ile Ala Thr Gln Tyr Leu Thr Asn Arg Ala
            180                 185                 190

Glu His Asp Arg Ile Ala Arg Gln Trp Thr Lys Arg Tyr Ala Thr
        195                 200                 205
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<212> PRT
<213> Homo sapiens

<400> 6

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Met Ala Asn Ile Ala Val Gln Arg Ile Lys Arg Glu Phe Lys Glu Val
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Leu Lys Ser Glu Glu Thr Ser Lys Asn Gln Ile Lys Val Asp Leu Val
            20                  25                  30

Asp Glu Asn Phe Thr Glu Leu Arg Gly Glu Ile Ala Gly Pro Pro Asp
        35                  40                  45

Thr Pro Tyr Glu Gly Gly Arg Tyr Gln Leu Glu Ile Lys Ile Pro Glu
     50                  55                  60

Thr Tyr Pro Phe Asn Pro Pro Lys Val Arg Phe Ile Thr Lys Ile Trp
 65                  70                  75                  80

His Pro Asn Ile Ser Ser Val Thr Gly Ala Ile Cys Leu Asp Ile Leu
                 85                  90                  95

Lys Asp Gln Trp Ala Ala Ala Met Thr Leu Arg Thr Val Leu Leu Ser
            100                 105                 110
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Leu Gln Ala Leu Leu Ala Ala Ala Glu Pro Asp Asp Pro Gln Asp Ala
        115                 120                 125

Val Val Ala Asn Gln Tyr Lys Gln Asn Pro Glu Met Phe Lys Gln Thr
    130                 135                 140

Ala Arg Leu Trp Ala His Val Tyr Ala Gly Ala Pro Val Ser Ser Pro
145                 150                 155                 160

Glu Tyr Thr Lys Lys Ile Glu Asn Leu Cys Ala Met Gly Phe Asp Arg
                165                 170                 175

Asn Ala Val Ile Val Ala Leu Ser Ser Lys Ser Trp Asp Val Glu Thr
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Ala Thr Glu Leu Leu Leu Ser Asn
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<210> 7
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<213> Drosophila melanogaster

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Met Arg Ser Glu Glu Ile Val Gln Cys Ser Ile Lys Ile Glu Leu Val
             20                  25                  30

Asn Asp Ser Trp Thr Glu Leu Arg Gly Glu Ile Ala Gly Pro Pro Asp
         35                  40                  45

Thr Pro Tyr Glu Gly Gly Lys Phe Val Leu Glu Ile Lys Val Pro Glu
     50                  55                  60

Thr Tyr Pro Phe Asn Pro Pro Lys Val Arg Phe Ile Thr Arg Ile Trp
 65                  70                  75                  80

His Pro Asn Ile Ser Ser Val Thr Gly Ala Ile Cys Leu Asp Ile Leu
                85                  90                  95

Lys Asp Asn Trp Ala Ala Ala Met Thr Leu Arg Thr Val Leu Leu Ser
            100                 105                 110

Leu Gln Ala Leu Leu Ala Ala Ala Glu Pro Asp Asp Pro Gln Asp Ala
        115                 120                 125

Val Val Ala Tyr Gln Phe Lys Asp Lys Tyr Asp Leu Phe Leu Leu Thr
    130                 135                 140

Ala Lys His Trp Thr Asn Ala Tyr Ala Gly Gly Pro His Thr Phe Pro
145                 150                 155                 160

Asp Cys Asp Ser Lys Ile Gln Arg Leu Arg Asp Met Gly Ile Asp Glu
                165                 170                 175
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His Glu Ala Arg Ala Val Leu Ser Lys Glu Asn Trp Asn Leu Glu Lys
            180                 185                 190

Ala Thr Glu Gly Leu Phe Ser
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<212> PRT
<213> Saccharomyces cerevisiae

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Met Ser Ser Arg Lys Ser Thr Ala Ser Ser Leu Leu Leu Arg Gln Tyr
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Arg Glu Leu Thr Asp Pro Lys Lys Ala Ile Pro Ser Phe His Ile Glu
             20                  25                  30

Leu Glu Asp Asp Ser Asn Ile Phe Thr Trp Asn Ile Gly Val Met Val
         35                  40                  45

Leu Asn Glu Asp Ser Ile Tyr His Gly Gly Phe Phe Lys Ala Gln Met
     50                  55                  60

Arg Phe Pro Glu Asp Phe Pro Phe Ser Pro Pro Gln Phe Arg Phe Thr
 65                  70                  75                  80

Pro Ala Ile Tyr His Pro Asn Val Tyr Arg Asp Gly Arg Leu Cys Ile
                85                  90                  95

Ser Ile Leu His Gln Ser Gly Asp Pro Met Thr Asp Glu Pro Asp Ala
            100                 105                 110

Glu Thr Trp Ser Pro Val Gln Thr Val Glu Ser Val Leu Ile Ser Ile
        115                 120                 125

Val Ser Leu Leu Glu Asp Pro Asn Ile Asn Ser Pro Ala Asn Val Asp
    130                 135                 140

Ala Ala Val Asp Tyr Arg Lys Asn Pro Glu Gln Tyr Lys Gln Arg Val
145                 150                 155                 160

Lys Met Glu Val Glu Arg Ser Lys Gln Asp Ile Pro Lys Gly Phe Ile
                165                 170                 175

Met Pro Thr Ser Glu Ser Ala Tyr Ile Ser Gln Ser Lys Leu Asp Glu
            180                 185                 190

Pro Glu Ser Asn Lys Asp Met Ala Asp Asn Phe Trp Tyr Asp Ser Asp
        195                 200                 205

Leu Asp Asp Asp Glu Asn Gly Ser Val Ile Leu Gln Asp Asp Asp Tyr
    210                 215                 220

Asp Asp Gly Asn Asn His Ile Pro Phe Glu Asp Asp Asp Val Tyr Asn
225                 230                 235                 240
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Tyr Asn Asp Asn Asp Asp Asp Asp Glu Arg Ile Glu Phe Glu Asp Asp
245 250 255

Asp Asp Asp Asp Asp Asp Ser Ile Asp Asn Asp Ser Val Met Asp Arg
260 265 270

Lys Gln Pro His Lys Ala Glu Asp Glu Ser Glu Asp Val Glu Asp Val
275 280 285

Glu Arg Val Ser Lys Lys Ile
290 295

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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tgcagtgtct ggctcggtgc 20

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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ctgatctgca tgatcactga c 21

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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tccactgcaa catcacggag tcataccctg 30

<210> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12
atgcagtcga actcgtgaat gacagtctgt 30

<210> 13
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<212> DNA
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<223> Description of Artificial Sequence: Primer

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gcagcagcgg ccgcgacgag ctgagctgcg agttcctgc 39

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<223> Description of Artificial Sequence: Primer

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gcagcagtcg acgccgtctt cttttggggg tgtgtac 37

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<223> Description of Artificial Sequence: Primer

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<212> PRT
<213> Homo sapiens

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His Cys Asn Ile Thr Glu Ser Tyr Pro Ala Val Pro Pro Ile Trp Ser
20 25 30

Val Glu Ser Asp Asp Pro Asn Leu Ala Ala Val Leu Glu Arg Leu Val
35 40 45

Asp Ile Lys Lys Gly Asn Thr Leu Leu Leu Gln His Leu Lys Arg Ile
50 55 60

Ile Ser Asp Leu Cys Lys Leu Tyr Asn Leu Pro Gln His Pro Asp Val
65 70 75 80

Glu Met Leu Asp Gln Pro Leu Pro Ala Glu Gln Cys Thr Gln Glu Asp
85 90 95

Val Ser Ser Glu Asp Glu Asp Glu Glu Met Pro Glu Asp Thr Glu Asp
100 105 110

Leu Asp His Tyr Glu Met Lys Glu Glu Glu Pro Ala Glu Gly Lys Lys
115 120 125

Ser Glu Asp Asp Gly Ile Gly Lys Glu Asn Leu Ala Ile Leu Glu Lys
130 135 140

Ile Lys Lys Asn Gln Arg Gln Asp Tyr Leu Asn Gly Ala Val Ser Gly
145 150 155 160

Ser Val Gln Ala Thr Asp Arg Leu Met Lys Glu Leu Arg Asp Ile Tyr
165 170 175

Arg Ser Gln Ser Phe Lys Gly Gly Asn Tyr Ala Val Glu Leu Val Asn
180 185 190

Asp Ser Leu Tyr Asp Trp Asn Val Lys Leu Leu Lys Val Asp Gln Asp
195 200 205

Ser Ala Leu His Asn Asp Leu Gln Ile Leu Lys Glu Lys Glu Gly Ala
210 215 220

Asp Phe Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro Phe Asp
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Pro Pro Phe Val Arg
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<210> 18
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<210> 19
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<400> 19
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1 5 10

<210> 20
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<400> 20
Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro Phe
1 5 10

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<400> 26
Glu Leu Val Asn Asp Ser Leu Tyr Asp Trp Asn Val Lys Leu
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<210> 27
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Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro Phe Asp
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<210> 28
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<400> 28
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<210> 29
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<400> 29
Ala Val Glu Leu Val Asn Asp Ser Leu Tyr Asp Trp Asn Val
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<210> 30
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<400> 31
Val Gln Phe Gly Ala Asn Lys Ser Gln Tyr Ser Leu Thr Arg
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<400> 32
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<400> 33
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<210> 42
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Gly Tyr Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr Lys
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<400> 46
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<210> 47
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<212> PRT
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Tyr Arg Ser Gln Ser Phe Lys Gly Gly Asn Tyr Ala Val Glu Leu Val
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Asn Asp Ser Leu Tyr Asp Trp Asn Val Lys Leu Leu Lys Val Asp Gln
        35   40   45

Asp Ser Ala Leu His Asn Asp Leu Gln Ile Leu Lys Glu Lys Glu Gly
    50   55   60

Ala Asp Phe Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro Phe
65   70   75   80

Asp Pro Pro Phe Val Arg Val Val Ser Pro Val Leu Ser Gly Gly Tyr
                85   90   95

Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr Lys Gln Gly
            100   105   110

Trp Ser Ser Ala Tyr Ser Ile Glu Ser Val Ile Met Gln Ile Ser Ala
        115   120   125

Thr Leu Val Lys Gly Lys Ala Arg Val Gln Phe Gly Ala Asn Lys Ser
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Gln Tyr Ser Leu Thr Arg Ala Gln Gln Ser Tyr Lys Ser Leu Val Gln
145   150   155   160

Ile His Glu Lys

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<220>
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<210> 49
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<220>
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<400> 49
caagggttga tccagcatct 20

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<400> 50
atgaggcttg gatcagcttt 20

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<223> Description of Artificial Sequence: Primer

<400> 51
cctgaagcct gacattccat 20

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actgcagccg attcattaat g 21

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